

Table S1 *Rhizophagus irregularis* isolates selected for ddRAD-seq and amplicon sequencing

Isolate	Origin	Microsatellite genotype	ddRAD sequencing	Amplicon sequencing
A1	Tänikon, CH	IV	✓	-
A2	Tänikon, CH	XVIII	✓	-
A4	Tänikon, CH	XVII	✓	-
A5	Tänikon, CH	VII	✓	-
B1	Tänikon, CH	IX	✓	-
B2	Tänikon, CH	I	✓	-
B3	Tänikon, CH	II	✓	-
B4	Tänikon, CH	III	✓	-
B10	Tänikon, CH	I	✓	-
B12	Tänikon, CH	XIII	✓	-
B15	Tänikon, CH	VII	✓	-
C1	Tänikon, CH	XV	✓	-
C2	Tänikon, CH	XV	✓	✓
C3	Tänikon, CH	XVII	✓	✓
C4	Tänikon, CH	XVII	✓	-
C5	Tänikon, CH	XVI	✓	✓
DAOM 197198	Pont-Rouge, Canada	XII	✓	✓
D1	Tänikon, CH	VIII	✓	-
D3	Tänikon, CH	VI	✓	-
D4	Tänikon, CH	II	✓	-

Notes:

- CH = Switzerland

- Microsatellite genotypes are described in:

Croll D, Wille L, Gamper HA, Mathimaran N, Lammers PJ, Corradi N, Sanders IR.

2008. Genetic diversity and host plant preferences revealed by simple sequence repeat and mitochondrial markers in a population of the arbuscular mycorrhizal fungus *Glomus intraradices*. New Phytol. 178:672-687.

Table S2 Origin of data of reference species studied.

Species	Strain/ “Cultivar”	Ploidy	Origin of the sequencing data	Reference
<i>Saccharomyces cerevisiae</i>	S288C	n	This study	NCBI link
<i>Schizosaccharomyces pombe</i>	972h-	n	This study	NCBI link
<i>Candida albicans</i>	DSY294 (C43)	2n	This study	Sanglard et al. 1998
<i>Candida albicans</i>	SC5314	2n	This study	NCBI link
<i>Betula nana</i>	097-10	2n	Public data	Wang et al. 2013
<i>Betula nana</i>	582	2n	Public data	Wang et al. 2013
<i>Betula × intermedia</i>	1123	4n	Public data	Wang et al. 2013
<i>Betula × intermedia</i>	1045	4n	Public data	Wang et al. 2013
<i>Betula × intermedia</i>	325	4n	Public data	Wang et al. 2013
<i>Betula pubescens</i>	425f	4n	Public data	Wang et al. 2013
<i>Betula pubescens</i>	605p	4n	Public data	Wang et al. 2013
<i>Betula pendula</i> hybrid?	1184c	4n	Public data	Wang et al. 2013

- Sanglard D, Ischer F, Calabrese D, de Micheli M, Bille J. 1998. Multiple resistance mechanisms to azole antifungals in yeast clinical isolates. Drug Resist Update. 1:255-265.

- Wang N, Thomson M, Bodles WJA, Crawford RMM, Hunt HV, Featherstone AW, Pellicer J, Buggs RJA. 2013. Genome sequence of dwarf birch (*Betula nana*) and cross-species RAD markers. Mol Ecol. 22:3098-3111.

Table S3 Genome characteristics of *Rhizophagus irregularis*, *Candida albicans* and *Betula nana*

	fungus <i>Candida albicans</i>	fungus <i>Rhizophagus irregularis</i>	plant <i>Betula nana</i>
Strain, isolate or variety	SC5314	DAOM197198	097-10
Version	A21-s02-m08-r09	N6 as in Lin et al. 2014	as in Wang et al. 2013
Number of scaffolds	9	12603	551915
Assembled genome size (Mb)	14.3	115.1	564.0
% Repeated	4%	30%	34%
% Coding	62%	31%	15%
Total number of predicted ddRAD-seq fragments	6427	36235	88374
% Predicted ddRAD-seq fragments that can not be mapped	1%	1%	8%
% Predicted ddRAD-seq fragments that form cluster of repeated sequences	3%	12%	13%

Table S4 List of loci selected for amplicon sequencing, primer sequences and expected PCR product sequences.

Croll D, Willis L, Gamper HA, Mathimaran N, Lammers PJ, Corradi N, Sanders IR. 2008. Genetic diversity and host plant preferences revealed by simple sequence repeat and mitochondrial markers in a population of the arbuscular mycorrhizal fungus *Glomus intraradices*. New Phytol. 178:672-687.

Table S5 Details of ddRAD-seq data on *Rhizophagus irregularis* isolates and reference species.

Samples include 20 isolates of *Rhizophagus irregularis*, 2 strains of *Candida albicans*, 1 strain of *Saccharomyces cerevisiae*, 1 strain of *Schizosaccharomyces pombe* and 8 *Betula* spp. individuals. The last row shows the average per column for *R. irregularis* samples only.

Sample name	Number of retained sequence reads	Number of ddRAD-seq loci covered by at least 10 sequence reads	Number of absent ddRAD-seq loci (no reads)	Mean coverage per ddRAD-seq locus (only loci with coverage ≥ 10)	Number of monoallelic SNPs compared to reference genome	Number of monoallelic indels compared to reference genome	Number of poly-allelic sites (SNPs or indels)
For <i>R. irregularis</i> and yeast samples, the number to the right of the dash indicates the biological replicate number	See Materials and Methods for details on read quality filtering and demultiplexing	ddRAD-seq loci were predicted <i>in silico</i> , see Materials and Methods and Table S3 for details	These are the loci that were covered in other samples but not in that particular sample	SNPs obtained after variant calling against the reference genome. Numbers differ among replicates because not all SNPs were covered at a minimum of 10x in all replicates. However, consistency of SNPs among replicates was high (See Table S7)	Indels obtained after variant calling against the reference genome. Numbers differ among replicates because not all indels were covered at a minimum of 10x in all replicates.	Poly-allelic sites obtained after variant calling against the reference genome. Numbers differ among replicates because not all sites were recorded as poly-allelic at a minimum of 10x coverage in all replicates. See Table S7 and Figure S2 for consistency of poly-allelic SNPs among replicates.	
A1-1	1 706 945	20 579	5 837	37	7 264	1 320	5 302
A1-2	1 522 470	18 605	6 534	36	6 718	1 181	5 276
A1-3	1 227 961	17 058	6 790	30	5 799	1 012	4 481
A2-1	1 823 153	15 343	11 329	39	14 823	3 074	6 003
A2-2	908 899	10 841	12 894	26	9 526	1 965	4 590
A2-3	1 380 536	13 150	11 780	32	11 824	2 304	5 372
A4-1	1 366 305	14 288	11 237	32	12 179	2 357	6 770
A4-2	1 644 519	15 109	10 137	38	11 848	2 242	8 249
A4-3	1 578 489	15 913	9 915	33	13 163	2 696	8 076
A5-1	1 485 896	19 735	5 858	33	6 004	930	7 269
A5-2	1 398 378	17 618	6 822	35	5 680	913	6 841
A5-3	1 713 425	19 570	5 955	38	6 224	960	7 466
B1-1	1 669 030	18 611	6 527	39	6 564	1 141	5 284
B1-2	1 520 684	16 847	8 082	41	6 818	1 181	4 885
B1-3	1 648 990	19 196	6 350	37	6 936	1 142	5 242
B2-1	1 605 804	16 940	6 763	40	5 867	967	5 293
B2-2	1 669 925	17 116	6 856	41	6 274	1 030	4 857
B2-3	1 121 733	15 082	10 208	33	6 392	1 044	5 064
B3-1	1 832 680	19 011	6 584	43	7 075	1 126	5 463
B3-2	1 266 390	16 366	7 745	35	6 234	925	5 519
B3-3	2 080 625	20 259	6 161	45	7 394	1 192	5 826
B4-1	1 251 024	16 021	8 054	33	6 422	1 134	5 121
B4-2	2 025 045	20 750	5 949	41	7 932	1 310	5 852
B4-3	1 751 009	19 950	5 780	38	6 638	1 029	6 717
B10-1	1 511 526	17 377	6 363	37	5 514	933	6 030
B10-2	1 472 787	17 802	6 824	36	6 133	997	4 914
B10-3	1 493 727	17 595	6 860	36	6 490	1 073	5 052
B12-1	1 550 617	16 868	7 730	41	6 722	1 079	5 788
B12-2	2 171 314	20 673	5 796	44	7 597	1 206	6 050
B12-3	1 815 575	20 786	5 431	37	6 306	1 041	8 864
B15-1	1 777 696	20 792	5 546	37	6 670	1 079	8 005
B15-2	1 917 296	18 861	6 700	44	7 119	1 223	8 092
B15-3	1 875 268	20 747	5 569	40	6 501	1 043	8 194
C1-1	1 428 591	14 644	9 646	38	8 698	1 488	6 119
C1-2	1 590 777	15 572	9 196	37	9 496	1 505	6 117
C1-3	1 572 111	15 896	9 659	37	9 822	1 583	5 706
C2-1	2 007 830	17 250	9 019	42	11 098	1 940	5 964
C2-2	1 353 515	13 584	11 239	37	9 613	1 704	5 260
C2-3	1 559 213	14 895	9 157	38	8 739	1 381	6 227
C3-1	1 195 108	12 522	11 173	34	9 644	1 873	9 091
C3-2	1 650 771	15 294	10 737	37	13 175	2 476	7 387
C3-3	1 602 764	15 351	9 871	35	12 513	2 440	8 612
C4-1	1 537 303	15 618	10 848	33	13 244	2 584	7 259
C4-2	1 762 563	16 577	9 902	35	13 781	2 701	8 112
C4-3	1 507 330	14 512	10 244	33	11 406	2 103	7 598
C5-1	1 854 852	16 816	9 003	42	10 597	1 865	6 314
C5-2	1 435 722	14 702	9 050	36	8 678	1 551	6 731
C5-3	1 411 395	14 705	9 714	34	8 906	1 421	5 574
D1-1	1 665 050	19 084	6 404	37	7 140	1 192	5 326
D1-2	2 000 672	20 327	6 002	40	7 830	1 386	5 533
D1-3	2 006 019	21 415	5 673	39	7 681	1 313	5 544
D3-1	1 584 204	18 424	6 703	37	6 927	1 136	5 156
D3-2	1 441 512	17 141	7 219	37	6 370	1 019	5 458
D3-3	1 653 318	18 498	5 878	38	5 959	990	6 055
D4-1	1 322 125	15 411	8 541	38	6 371	1 046	4 987
D4-2	1 617 737	18 098	6 713	38	6 363	1 014	4 910
D4-3	1 614 094	17 997	6 756	38	6 538	1 025	5 167
DAOM 197198-1	1 118 839	16 584	5 042	32	225	60	3 081
DAOM 197198-2	850 460	14 551	6 429	27	208	51	2 922
DAOM 197198-3	1 200 297	17 518	5 707	34	274	73	3 185
DAOM 197198-4	1 523 828	20 259	3 066	37	231	74	3 275
DAOM 197198-5	1 412 756	19 662	3 020	33	227	58	3 428
<i>C. albicans</i> DSY294-1	1 389 605	5 375	152	121	2 264	176	3 670
<i>C. albicans</i> DSY294-2	734 552	4 978	172	67	2 106	154	3 428
<i>C. albicans</i> DSY294-3	1 425 647	5 258	172	144	2 304	170	3 650
<i>C. albicans</i> SC5314-1	465 736	4 461	134	48	140	8	2 397
<i>C. albicans</i> SC5314-2	1 867 362	5 629	51	158	226	15	2 970
<i>C. albicans</i> SC5314-3	1 772 070	5 838	26	135	191	15	3 000
<i>S. cerevisiae</i> S288C-1	2 095 437	NA*	NA*	NA*	796	52	0
<i>S. cerevisiae</i> S288C-2	972 533	NA	NA	NA	734	42	0
<i>S. pombe</i> 972h-1	466 545	NA	NA	NA	19	4	0
<i>S. pombe</i> 972h-2	440 349	NA	NA	NA	22	3	0
<i>Betula</i> mana-097-10**	3 420 901	48 769	9 091	69	2 120	191	19 938
<i>Betula</i> x <i>intermedia</i> -325	2 810 615	40 372	30 425	69	14 886	1 634	48 690
<i>Betula</i> pubescens-425f	2 167 545	39 438	29 461	54	14 883	1 589	48 238
<i>Betula</i> mana-582	1 282 265	34 764	33 086	35	10 516	1 247	15 201
<i>Betula</i> pubescens-605p	1 464 762	35 599	30 277	40	13 602	1 402	46 117
<i>Betula</i> x <i>intermedia</i> -1123	4 434 021	42 645	28 459	103	16 223	1 702	51 102
<i>Betula</i> x <i>intermedia</i> -1045	1 112 021	32 184	32 334	32	12 052	1 251	42 708
<i>Betula pendula</i> hybrid-1184c	1 621 764	36 688	30 913	43	14 476	1 506	44 786

For <i>R. irregularis</i> samples:	Number of retained sequence reads	Number of ddRAD-seq loci covered by at least 10 sequence reads	Number of absent ddRAD-seq loci (no reads)	Mean coverage per ddRAD-seq locus (only loci with coverage ≥ 10)	Number of monoallelic SNPs compared to reference genome	Number of monoallelic indels compared to reference genome	Number of poly-allelic sites (SNPs or indels)
Minimum	850 460	10 841	3 020	26	208	51	2 922
Maximum	2 171 314	21 415	12 894	45	14 823	3 074	9 091
Average/sample	1 568 814	17 232	7 719	37	7 619	1 337	5 934

* Because no poly-allelic positions were detected in *S. cerevisiae* and *S. pombe*, we did not generate files for these samples for further analyses after SNP calling, so we did not calculate details of RAD-seq locus numbers and coverage for these samples

** All *Betula* spp. reads were obtained from Wang N, Thomson M, Bodies WJA, Crawford RMM, Hunt HV, et al. (2013) Genome sequence of dwarf birch (*Betula nana*) and cross-species RAD markers. Molecular Ecology 22: 3098-3111

Table S6 Density of SNPs among *Rhizobius irregularis* isolates in non-repeated – coding regions. Sites with mono-allelic SNPs were compared between all pairs of biological replicates. When the nucleotide was not the same at a site between the 2 replicates, it was recorded as a SNP between the replicates. The density of SNPs is expressed as number of SNPs/kb. SNP density values are displayed within a color-coded heatmap (lowest to highest values are highlighted by a green to red color gradient). DAOM = DAOM 197198

Table S7 Consistency among biological replicates in non-repeated regions (also see Supplementary Results for a description of how consistency was determined)

Isolate / Strain ¹	Mono-allelic SNPs					Poly-allelic SNPs							
	Number of SNP sites consistent among all replicates ²	Number of consistent SNP sites with missing information in 1 of the replicates ³	Number of SNP sites with missing information in 2 of the replicates ⁴	Number of SNP sites inconsistent among replicates ⁵	Inconsistency level ⁶	Number of poly-allelic sites consistent among all replicates ⁷	Number of consistent poly-allelic sites with missing information in 1 of the replicates ⁸	Number of poly-allelic sites with missing information in 2 of the replicates ⁹	Number of poly-allelic sites with a missing allele in 1 of the replicates (no 'na' site included) ¹⁰	Number of poly-allelic sites inconsistent among replicates ¹¹	Number of undetermined types of poly-allelic sites (containing 'na' or unsolvable) ¹²	Inconsistency level ¹³	
A1	3039	730	844	15	0.5%	763	201	240	75	8	244	10.9%	
A2	5994	2123	2175	40	0.7%	884	343	401	124	21	594	16.4%	
A4	6398	1641	1841	32	0.5%	1498	423	542	238	24	1300	17.5%	
A5	2756	576	621	15	0.5%	1449	399	449	118	9	200	8.8%	
B1	3175	626	673	10	0.3%	848	199	204	91	6	288	11.4%	
B2	2670	637	785	7	0.3%	751	180	210	92	12	443	13.8%	
B3	3175	688	620	18	0.6%	980	216	160	97	16	345	11.5%	
B4	2676	1242	733	28	1.0%	823	327	288	115	10	770	15.2%	
B10	2537	598	605	13	0.5%	822	165	197	113	15	633	15.6%	
B12	2749	681	812	23	0.8%	1084	229	248	291	26	1097	29.2%	
B15	3014	717	767	14	0.5%	1719	462	529	144	9	398	8.9%	
DAOM 197198	43	4	2	4	9.3%	477	66	42	30	3	222	6.9%	
C1	4393	1027	950	36	0.8%	1013	190	229	141	18	798	15.7%	
C2	4438	1506	1172	17	0.4%	991	223	176	138	9	691	14.8%	
C3	5351	1542	1673	30	0.6%	1498	496	486	359	25	2449	25.6%	
C4	6769	1888	1642	18	0.3%	1524	470	510	178	18	875	12.9%	
C5	4112	1240	1153	24	0.6%	988	219	252	145	10	1159	15.7%	
D1	3412	967	673	8	0.2%	866	236	204	122	8	336	15.0%	
D3	2711	508	572	8	0.3%	956	163	190	113	11	842	13.0%	
D4	2894	720	680	7	0.2%	910	208	152	91	5	225	10.5%	
DSY294	1972	143	94	8	0.4%	2570	346	199	44	10	74	2.1%	
SC5314	123	53	19	0	0.0%	1680	688	197	30	0	51	1.8%	

¹This analysis was not performed on haploid yeast and *Betula* spp.

²corresponds to sites where mono-allelic SNPs were detected by variant calling against the reference genome, and identical SNPs were found in all replicates of an isolate/strain.

³corresponds to sites where mono-allelic SNPs were detected and identical in some of the replicates, but with missing information (na) in one of the replicates.

⁴corresponds to sites where mono-allelic SNPs were detected, but with missing information (na) in two of the replicates. The accuracy of these SNPs cannot be determined in isolates represented by three biological replicates.

⁵corresponds to sites where mono-allelic SNPs were detected, but the SNPs were not identical among all replicates; See Supplementary Results for an example.

⁶corresponds to the number of SNP sites inconsistent between replicates divided by the number of SNP sites consistent among all replicates

⁷corresponds to sites where poly-alleles were detected and identical in all replicates of an isolate.

⁸orresponds to sites where poly-alleles were and identical in some of the replicates, but with missing information (na) in one of the replicates.

⁹corresponds to sites where poly-alleles were detected in at least one replicate, and where 2 replicates had missing information (na).

¹⁰corresponds to sites where poly-alleles were detected in at least one replicate, and where one of the alleles was not found in one of the replicates (only sites without missing information (na)); See Supplementary Results for an example

¹¹corresponds to sites where poly-alleles were detected in at least one isolate/strain, but the replicates had different allelic composition (inconsistent); See Supplementary Results for an example.

¹²corresponds to sites where poly-alleles were detected in at least one isolate/strain, but sites were complex or unclear (i.e. at least 2 replicates have 'na' or sites are inconsistent and have 'na')

¹³corresponds to the number of poly-allelic sites inconsistent or with missing alleles between replicates divided by the number of poly-allelic sites consistent among all replicates

Table S8 Percentage (%) of alleles at poly-allelic sites (SNPs only) found a specific number of times (x) in each individual replicate. Poly-allelic SNPs in all genomic regions are included (repeated/non-repeated and coding/non-coding).

Sample	All poly-allelic SNPs											Poly-allelic SNPs found in all replicates of each isolate										
	1x	2x	3x	4x	5x	6x	7x	8x	9x	10x	>10	1x	2x	3x	4x	5x	6x	7x	8x	9x	10x	>10
A1-1	0.52	2.46	2.35	3.40	3.10	3.13	3.28	3.50	3.06	3.26	71.9	0.05	0.30	0.75	1.25	1.33	1.87	1.86	2.61	2.40	2.55	85.0
A1-2	1.10	3.02	3.54	3.75	3.43	3.35	2.71	3.43	3.55	3.86	68.2	0.17	0.77	1.28	1.70	2.31	2.73	2.37	2.88	3.20	3.27	79.3
A1-3	0.25	1.40	2.98	3.45	4.01	4.48	5.22	4.25	4.33	4.13	65.5	0.17	0.71	1.70	2.53	3.47	4.16	4.59	4.22	4.37	4.07	70.0
A2-1	0.40	2.25	2.65	3.51	2.85	3.02	3.20	3.61	3.02	3.32	72.2	0.00	0.23	0.53	1.04	0.95	1.62	1.39	1.59	1.84	2.42	88.4
A2-2	0.95	3.48	4.09	4.66	4.53	4.55	5.13	4.19	4.40	4.99	59.0	0.12	0.92	2.79	3.86	4.73	4.39	5.55	4.29	4.76	5.08	63.5
A2-3	0.91	3.32	3.16	3.35	4.20	3.49	3.80	3.66	3.60	3.29	67.2	0.02	0.35	1.07	1.59	2.42	2.71	3.14	2.99	3.01	2.56	80.2
A4-1	0.30	1.46	3.29	4.18	4.16	3.82	4.50	4.35	4.73	4.53	64.7	0.06	0.55	2.02	2.75	3.10	3.13	3.86	3.64	4.21	4.23	72.5
A4-2	1.30	5.76	4.33	3.99	3.20	3.22	3.44	3.49	3.71	3.77	63.8	0.09	0.33	1.35	2.22	2.55	2.81	3.29	3.33	3.70	3.63	76.7
A4-3	0.93	4.09	3.42	3.87	3.68	3.60	4.68	4.51	3.98	3.77	63.5	0.13	0.48	1.37	2.22	2.87	2.95	3.87	3.96	3.75	3.70	74.7
A5-1	0.21	1.17	2.69	3.81	3.62	4.05	4.59	4.90	4.07	4.11	66.8	0.02	0.48	1.29	2.05	2.09	2.85	3.51	3.54	3.58	3.86	76.7
A5-2	0.24	1.33	2.49	3.71	4.10	4.06	4.87	4.40	4.12	3.62	67.1	0.08	0.66	1.33	2.62	3.25	3.38	4.25	3.95	3.85	3.59	73.0
A5-3	0.27	1.04	2.56	3.53	3.67	3.68	4.03	4.05	3.81	3.70	69.6	0.05	0.38	1.02	1.57	2.15	2.02	2.18	2.83	2.86	3.20	81.7
B1-1	1.96	3.09	3.52	3.42	3.12	2.83	2.97	3.30	3.18	3.65	69.0	0.17	0.73	1.34	2.24	2.31	2.63	2.90	3.21	2.81	3.41	78.3
B1-2	0.32	1.57	2.75	2.72	3.02	3.41	2.71	3.28	3.59	2.36	74.3	0.03	0.54	1.43	1.54	2.07	2.41	2.30	2.78	3.11	2.15	81.6
B1-3	0.34	1.20	2.58	3.38	2.78	3.32	3.40	3.66	3.43	3.54	72.4	0.03	0.30	1.08	1.63	1.50	2.11	2.47	2.85	3.02	3.18	81.8
B10-1	0.96	5.03	5.18	4.70	3.56	3.00	3.00	3.03	3.02	3.00	65.5	0.07	0.58	1.31	2.00	2.42	2.54	2.81	2.91	3.01	2.97	79.4
B10-2	0.57	1.92	2.77	3.14	3.13	3.71	3.86	3.86	3.30	2.73	71.0	0.14	0.30	1.21	1.82	2.42	3.23	3.52	3.13	2.65	2.44	79.1
B10-3	0.25	1.18	2.74	2.83	2.94	3.57	3.20	3.21	3.61	3.07	73.4	0.00	0.25	1.01	1.36	1.99	2.70	2.37	2.54	3.03	2.62	82.1
B12-1	1.73	3.62	2.81	2.96	2.34	2.37	2.48	2.61	2.69	2.64	73.7	0.26	0.86	1.06	1.89	1.92	2.13	2.47	2.43	2.36	2.66	82.0
B12-2	1.68	2.22	2.39	2.65	2.13	2.34	2.57	2.66	2.54	2.65	76.2	0.26	0.47	0.64	1.10	1.16	1.82	2.01	1.76	1.97	2.28	86.5
B12-3	0.78	2.25	3.50	3.76	3.78	3.39	4.41	4.54	4.23	4.02	65.3	0.16	0.65	0.74	1.31	2.13	1.80	2.71	2.95	2.78	2.92	81.9
B15-1	0.34	1.40	2.83	3.48	3.99	3.68	3.90	4.26	4.15	3.97	68.0	0.05	0.37	1.12	1.74	2.50	2.47	3.10	3.37	3.45	3.28	78.6
B15-2	0.16	1.07	2.37	2.64	2.96	3.59	3.11	3.57	3.59	3.47	73.5	0.04	0.42	1.08	1.48	1.88	2.32	2.36	2.75	2.72	2.89	82.0
B15-3	0.37	1.47	2.39	3.36	3.32	4.23	4.13	4.35	3.90	3.58	68.9	0.02	0.48	1.07	1.86	2.33	3.06	3.44	3.62	3.38	3.20	77.5
B2-1	0.57	3.11	4.91	3.87	3.60	3.17	3.05	3.15	3.69	3.13	67.8	0.08	0.43	1.79	2.05	2.36	1.99	2.62	2.68	3.24	2.64	80.1
B2-2	0.24	1.19	2.83	3.90	3.19	3.60	3.31	2.99	3.69	3.17	71.9	0.15	0.39	1.46	2.04	2.08	2.73	2.30	1.93	3.24	2.98	80.7
B2-3	1.69	2.45	2.94	2.63	2.37	3.46	2.96	2.84	2.92	2.75	73.0	0.43	0.57	1.53	1.48	1.46	2.39	2.24	2.41	2.51	2.74	82.2
B3-1	0.93	2.32	3.03	3.38	3.28	3.01	2.99	2.98	3.07	2.93	72.1	0.12	0.80	1.32	2.41	2.31	2.22	2.60	2.52	2.55	2.54	80.6
B3-2	1.88	3.30	2.46	3.01	3.25	2.99	2.63	3.08	3.45	3.44	70.5	0.17	1.06	1.03	1.63	2.71	2.89	2.45	3.06	3.35	3.23	78.4
B3-3	0.86	1.58	2.86	2.71	2.17	2.31	2.74	2.69	2.63	2.75	76.7	0.09	0.46	0.85	1.39	1.20	1.11	1.74	1.77	1.80	2.34	87.3
B4-1	2.11	3.07	3.29	3.15	3.52	3.89	3.32	3.86	3.91	3.54	66.3	0.47	1.46	2.06	2.69	3.15	3.90	3.29	4.24	4.14	3.39	71.2
B4-2	0.86	1.86	2.82	2.62	2.45	2.52	2.66	3.32	3.02	3.14	74.7	0.16	0.34	0.81	1.13	1.22	1.26	1.50	2.00	2.14	2.06	87.4
B4-3	2.83	4.57	3.60	3.02	2.67	2.99	2.60	2.48	2.98	3.19	69.1	0.18	0.45	0.68	1.26	1.59	2.34	2.11	1.77	2.17	2.14	85.3
C1-1	1.18	5.18	3.47	3.46	3.13	3.03	3.20	3.12	2.75	3.03	68.5	0.05	0.81	1.77	2.25	2.73	2.91	3.12	3.18	2.82	2.67	77.7
C1-2	0.71	2.79	3.31	3.10	3.22	3.69	2.80	3.33	3.62	3.32	70.1	0.06	0.33	1.37	1.79	1.91	2.89	2.20	2.90	3.20	2.98	80.4
C1-3	0.33	1.98	3.13	3.41	3.09	3.19	2.78	3.33	3.43	3.23	72.1	0.09	0.50	1.57	1.66	1.97	2.41	2.20	2.73	2.99	3.00	80.9
C2-1	0.46	2.22	2.48	3.33	2.69	3.11	3.50	2.99	2.65	3.20	73.4	0.04	0.39	1.13	1.19	1.26	1.97	1.99	2.11	1.83	2.68	85.4
C2-2	0.43	2.20	2.91	3.30	3.08	3.04	2.87	3.02	3.33	3.41	72.4	0.01	0.94	1.90	2.06	2.44	2.59	2.63	2.98	3.02	3.33	78.1
C2-3	1.45	5.06	4.07	3.92	2.73	3.05	2.79	3.11	3.14	3.26	67.4	0.03	0.59	1.71	2.74	3.10	4.07	3.81	4.19	4.75	4.08	70.9
C3-1	2.06	8.26	5.32	4.83	3.57	3.72	3.11	3.20	3.41	3.53	59.0	0.05	0.50	1.07	1.96	2.17	2.79	3.15	3.59	3.91	3.68	77.2
C3-2	0.34	1.51	2.63	3.77	3.42	3.86	4.22	4.33	4.39	4.25	67.3	0.03	0.70	1.82	2.56	2.43	2.83	3.29	3.19	2.95	3.29	76.9
C3-3	1.73	6.01	3.65	3.44	3.30	3.38	3.81	4.06	3.88	3.65	63.1	0.00	0.43	0.97	1.54	2.12	2.56	3.34	4.02	3.86	3.83	77.3
C4-1	0.41	1.42	2.91	3.43	3.78	4.73	4.53	4.78	4.36	4.83	64.8	0.08	0.58	1.56	2.29	3.00	3.75	3.61	4.25	3.93	4.39	72.5
C4-2	0.80	2.75	2.81	3.16	3.57	3.71	4.09	4.60	4.31	3.78	66.4	0.03	0.33	1.10	1.69	2.13	2.58	2.84	3.49	3.88	3.34	78.6
C4-3	1.28	5.03	3.40	4.21	3.52	4.11	3.91	4.30	4.32	4.04	61.9	0.02	0.51	1.47	3.32	2.94	4.01	3.89	4.72	4.51	4.20	70.4
C5-1	0.70	3.59	2.92	2.94	3.32	3.04	2.64	2.78	3.04	3.00	72.0	0.08	0.50	0.80	1.21	2.10	1.60	1.55	1.75	2.43	2.26	85.7
C5-2	1.82	6.95	4.70	3.85	2.90	2.93	3.01	2.84	3.00	3.34	64.7	0.03	0.70	1.82	2.56	2.43	2.83	3.29	3.19	2.95	3.29	76.9
C5-3	0.80	2.73	3.20	3.10	3.39	3.60	3.31	3.58	4.02	3.62	68.7	0.04	0.80	1.46	1.78	2.56	2.97	3.00	3.21	3.69	3.39	77.1
DAOM-1	0.20	1.25	2.78	3.50	2.91	2.84	3.28	2.66	3.17	3.15	74.3	0.05	0.12	0.50	1.03	1.						

Table S9 Number of ddRAD-seq loci with 1, 2, 3, 4 or ≥ 5 haplotypes per isolate.

Numbers represent number of loci in *Rhizopagrus irregularis* and *Candida albicans* isolates with 1 or more haplotypes averaged over 3-5 biological replicates. Haplotype numbers in *Betula* spp. samples were calculated from Wang et al. (2013). Loci are separated into genomic categories depending on whether they fall within non-repeated or repeated regions, and non-coding or coding regions.

Genomic region		Number of haplotypes	Rhizopagrus irregularis														
Repeated	Coding		DAOM 197198	A1	D1	B1	B2	D4	B3	B4	B10	D3	C2	B12	C1	C5	A2
no	no	1	11 269	8 206	8 993	7 850	6 537	6 934	7 875	8 017	7 067	7 397	6 234	7 897	6 168	6 220	5 074
		2	154	280	352	292	285	238	296	395	369	406	320	664	337	416	373
		3	55	58	62	51	59	57	65	87	69	61	54	111	56	61	74
		4	19	25	28	23	22	25	29	33	30	27	22	32	22	27	30
		≥ 5	46	17	21	20	17	23	30	20	21	26	23	34	24	21	30
	yes	1	14 097	9 204	9 981	9 182	8 152	8 718	9 194	9 057	8 610	9 064	7 887	9 237	7 761	7 820	6 750
		2	268	378	441	373	382	326	418	502	462	465	392	661	472	484	403
		3	103	113	126	103	110	123	138	134	125	123	102	159	117	125	152
		4	59	49	59	58	57	46	57	54	59	70	52	77	40	61	63
		≥ 5	86	53	59	67	71	66	68	74	69	75	104	92	104	95	64
yes	no	1	8 630	5 071	5 609	4 973	4 552	4 854	5 033	5 074	4 622	4 791	3 809	5 056	3 660	3 669	2 868
		2	264	338	427	327	325	277	375	453	358	472	313	601	312	375	333
		3	137	124	135	123	133	132	141	134	137	136	105	187	100	108	117
		4	60	51	81	50	48	66	67	64	54	69	65	83	56	75	65
		≥ 5	104	88	93	98	81	85	91	102	104	94	107	112	122	111	129
	yes	1	10 424	5 868	6 432	5 816	5 202	5 649	5 904	5 979	5 419	5 679	4 386	5 964	4 290	4 287	3 550
		2	692	660	731	609	605	570	697	741	667	711	558	948	533	614	463
		3	346	277	292	306	302	303	301	293	289	309	242	316	245	274	232
		4	179	178	163	179	177	178	182	177	178	178	163	139	210	158	153
		≥ 5	430	286	312	309	302	324	333	353	322	318	389	388	399	381	207

Genomic region		Number of haplotypes	Rhizopagrus irregularis					Betula spp.							Candida albicans		
Repeated	Coding		A5	B15	C4	A4	C3	097-10	582	1123	1045	325	425f	605p	1184c	DSY294	SC5314
no	no	1	7 251	8 004	5 611	5 316	4 817	9 797	9 062	5 026	5 165	5 075	5 128	5 111	5 284	874	1 142
		2	894	1 074	789	822	892	3 171	2 625	4 690	4 388	4 736	4 661	4 599	4 671	1 006	745
		3	107	135	134	161	163	293	202	2 016	1 818	1 970	1 979	1 968	1 768	99	88
		4	44	62	56	65	65	65	49	698	419	562	544	484	444	21	34
		≥ 5	36	42	55	50	54	51	24	360	110	238	189	135	137	4	5
	yes	1	8 596	9 207	7 520	7 168	6 654	10 863	10 673	5 975	6 319	6 173	6 110	6 277	6 365	2 685	3 396
		2	915	976	824	957	1 110	2 932	2 529	5 332	5 130	5 240	5 334	5 194	5 222	3 087	2 438
		3	163	203	206	214	242	248	132	1 699	1 524	1 658	1 726	1 627	1 563	172	130
		4	60	64	91	93	98	58	44	523	320	459	397	345	330	25	23
		≥ 5	84	107	91	84	100	28	13	243	69	149	122	104	104	1	0
yes	no	1	4 479	5 013	2 857	2 764	2 536	5 872	4 449	3 080	2 798	3 015	3 018	2 963	2 918	243	324
		2	741	867	520	502	585	2 163	1 297	2 278	1 871	2 158	2 190	2 110	2 062	261	210
		3	182	225	183	180	203	285	173	1 063	881	1 013	1 000	1 001	916	49	46
		4	91	101	95	103	110	104	43	418	262	356	360	273	275	24	13
		≥ 5	98	124	190	178	187	91	34	331	113	210	195	168	146	14	6
	yes	1	5 367	5 872	3 759	3 571	3 347	3 281	2 715	1 804	1 743	1 701	1 771	1 785	1 759	449	562
		2	1 007	1 151	848	873	857	1 120	750	1 354	1 238	1 356	1 327	1 301	1 336	511	418
		3	370	394	356	334	396	181	76	574	465	509	542	516	477	60	52
		4	202	196	150	160	164	71	18	210	117	207	196	161	135	9	10
		≥ 5	346	406	308	310	325	74	15	162	57	115	98	87	72	7	9

Table S10 Comparison between variants detected by ddRAD-seq and by amplicon sequencing at the same genomic locations in four isolates of *Rhizophagus irregularis*.

Rep=biological replicate; del=deletion.

Locus	Scaffold	Position	Variants found with ddRAD-seq												variants found with amplicon sequencing									
			DAOM197198					C02			C05			C03			DAOM197198		C02		C05		C03	
			rep1	rep2	rep3	rep4	rep5	rep1	rep2	rep3	rep1	rep2	rep3	rep1	rep2	rep3	rep1	rep2	rep1	rep2	rep1	rep2		
locus3	1	107369	C	C	C	C	C	C	C	C	C	C	C	C/T	C/T	C/T	C	C	C	C	I	I		
locus6	35	81678	T	T	T	T	T	C	C	C	C	C	C	T	T	T	T	T	A	A	G	G		
locus6	35	81697	A	A	A	A	A	A	A	A	A	A	A	G	G	G	G	G	A/G	A/G	A/G	A/G		
locus6	35	81741	G	G	G	G	G	G	G	G	G	G	G	A/G	A/G	A/G	A/G	A/G	C	C	C/T	C/T		
locus6	35	81767	C	C	C	C	C	C	C	C	C	C	C	C/T	C/T	C/T	C/T	C/T	C	C	C/T	C/T		
locus6	35	81769	C	C	C	C	C	del -1	C	C	C	C	C	C	C	C	C	C						
locus7	480	7320	A/G	na	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	G	G	G	A/G	A/G		
locus7	480	7326	T	T	T	T	T	T	T	T	T	T	T	G/T	G/T	G/T	G/T	T	T	T	T	T	T	
locus7	480	7332	C	C	C	C	C	C	C	C	C	C	C	C/T	C/T	C/T	C/T	C	C	C	C/T	C/T	C/T	
locus7	480	7347	G/T	na	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	G/T	T	T	T	T	T	T	
locus7	480	7366	A/G	na	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A/G	A	A	A	A	A	A	
locus8	845	17452	G	G	G	G	G	G	G	G	G	G	G	na	A/G	A/G	G	G	G	G	A/G	A/G	A/G	
locus8	845	17467	T	na	T	T	T	C/T	na	C/T	C/T	na	C/T	na	C	C	T	T	C/T	C/T	C/T	C	C	
locus8	845	17486	A	na	A	A	A	A/G	na	A/G	A/G	na	A/G	A/G	A/G	A/G	A	A	A/G	A/G	A/G	A/G	A/G	
locus8	845	17518	T	na	T	T	T	T	na	T	T	na	T	na	C	C	T	T	T	T	T	C	C	
locus8	845	17527	C	C	C	C	C	C/T	na	C/T	C/T	na	C/T	na	C	C	C	C	C/T	C/T	C	C	C	
locus8	845	17529	A	na	A	A	A	na	A	A	na	A	A	na	A/G	A/G	A	A	A	A	A/G	A/G	A/G	
locus8	845	17584	na	na	na	na	na	A/G	na	A/G	A/G	A/G	A/G	na	na	A	A	A	A/G	A/G	A	A	A	
locus8	845	17602	na	na	na	na	na	C/T	na	na	C/T	na	C/T	na	na	C	C	C/T	C/T	C/T	C	C	C	
locus10	1463	11466	T	T	T	T	T	T	T	T	T	T	T	A	A	A	T	T	T	T	A	A	A	
locus10	1463	11483	T	T	T	T	T	T	T	T	T	T	T	C/G	C/G	C/G	T	T	T	T	C/G	C/G	C/G	
locus10	1463	11511	T	T	T	T	T	T	T	T	T	T	T	G	G	G	T	T	T	T	T	G	G	
locus11	10	110544	na	na	na	na	na	A	A	A	A	A	A	G	G	G	G	G	G	A	A	G	G	
locus11	10	110565	na	na	na	na	na	C	C	C	C	C	C	C/T	C/T	C/T	C/T	C	C	C	C	C/T	C/T	
locus11	10	110578	na	na	na	na	na	C	C	C	C	C	C	T	T	T	T	C	C	C	C	T	T	
locus11	10	110654	na	na	na	na	na	G	G	G	G	G	G	A	A	A	G	G	G	G	A	A	A	